

# SEQUENCE PROTOCOL

<110> Degussa AG

<120> Nucleotide sequences which code for the sahH gene

<130> 000493 BT

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (227)..(1720)

<223> sahH gene

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tggaagaggc agatgtggaa tatgacctcg aagcttattt agaggccctc aactagccct 180

ccactaaaca gcttcaatca attcgggtgc cactccaaca tgtaga gtg gtg cgc 235

Met Val Arg

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gtt aaa aaa gtt ttc cta att ttc att ttc tta aaa gga gct cgc cag 283

Val Lys Lys Val Phe Leu Ile Phe Ile Phe Leu Lys Gly Ala Arg Gln

5

10

15

gac atg gca cag gtt atg gac ttc aag gtt gcc gat ctt tca cta gca 331

Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala

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30

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gag gca gga cgt cac cag att cgt ctt gca gag tat gag atg cca ggt 379

Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly

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ctc atg cag ttg cgc aag gaa ttc gca gac gag cag cct ttg aag ggc 427

Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly

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gcc cga att gct ggt tct atc cac atg acg gtc cag acc gcc gtg ctt 475

Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu

70

75

80

att gag acc ctc act gct ttg ggc gct gag gtt cgt tgg gct tcc tgc 523

Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys

85

90

95

aac att ttc tcc acc cag gat gag gct gca gcg gct atc gtt gtc ggc 571

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5	tcc ggc acc gtc gaa gag cca gct ggt gtt cca gta ttc gcg tgg aag Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys	619
	120 125 130	
10	ggt gag tca ctg gag gag tac tgg tgg tgc atc aac cag atc ttc agc Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser	667
	135 140 145	
15	tgg ggc gat gag ctg cca aac atg atc ctc gac gac ggc ggt gac gcc Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala	715
	150 155 160	
	acc atg gct gtt att cgc ggt cgc gaa tac gag cag gct ggt ctg gtt Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val	763
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	180 185 190	
25	atg ctg cgt gag gtt ctt gct gca gag cct ggc aag tgg ggc aag atc Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile	859
	200 205 210	
30	gct gag gcc gtt aag ggt gtc acc gag gaa acc acc acc ggt gtg cac Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His	907
	215 220 225	
35	cgc ctg tac cac ttc gct gaa gaa ggc gtg ctg cct ttc cca gcg atg Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met	955
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40	acc cgc cac tcc ctg atc gac ggc atc aac cgc gcc act gac atg ctc Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu	1051
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	280 285 290	
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	295 300 305	
	gaa gct gac cca atc aac gct ctt cag gct ctg atg gat ggc tac tct Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser	1195
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Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr  
325 330 335

5 ggc acc ggc aac aag gac atc att tcc ttc gag cag atg ctc aag atg 1291  
Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met  
340 345 350 355

10 aag gat cac gct ctg ctg ggc aac atc ggt cac ttt gat aat gag atc 1339  
Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile  
360 365 370

15 gat atg cat tcc ctg ttg cac cgc gac gac gtc acc cgc acc acg atc 1387  
Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile  
375 380 385

aag cca cag gtc gac gag ttc acc ttc tcc acc ggt cgc tcc atc atc 1435  
Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile  
390 395 400

20 gtc ctg tcc gaa ggt cgc ctg ttg aac ctt ggc aac gcc acc gga cac 1483  
Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His  
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25 cca tca ttt gtc atg tcc aac tct ttc gcc gat cag acc att ggc cag 1531  
Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln  
420 425 430 435

30 atc gaa ctg ttc caa aac gaa gga cag tac gag aac gag gtc tac cgt 1579  
Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg  
440 445 450

35 ctg cct aag gtt ctc gac gaa aag gtg gca cgc atc cac gtt gag gct 1627  
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455 460 465

40 ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag gct gag tac atc 1675  
Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile  
470 475 480

ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac tac cgc tac 1720  
Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr  
485 490 495

45 taatgattgt cagcattgag ggaatcgacg gcgccggcaa aaacaccctg gtttcggcat 1780  
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5 Ser Leu Ala Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu  
35 40 45

Met Pro Gly Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro  
50 55 60

10 Leu Lys Gly Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr  
65 70 75 80

Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp  
85 90 95

15 Ala Ser Cys Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile  
100 105 110

20 Val Val Gly Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe  
115 120 125

Ala Trp Lys Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln  
130 135 140

25 Ile Phe Ser Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly  
145 150 155 160

Gly Asp Ala Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala  
165 170 175

30 Gly Leu Val Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala  
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35 Phe Leu Gly Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp  
195 200 205

Gly Lys Ile Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr  
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40 Gly Val His Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe  
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Pro Ala Met Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn  
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45 Lys Tyr Gly Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr  
260 265 270

50 Asp Met Leu Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp  
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Val Gly Lys Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val  
290 295 300

55 Lys Val Thr Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp  
305 310 315 320

Gly Tyr Ser Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile  
325 330 335

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Val Ile Thr Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met  
340 345 350

5 Leu Lys Met Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp  
355 360 365

Asn Glu Ile Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg  
370 375 380

10 Thr Thr Ile Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg  
385 390 395 400

Ser Ile Ile Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala  
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15 Thr Gly His Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr  
420 425 430

Ile Ala Gln Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu  
435 440 445

20 Val Tyr Arg Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His  
450 455 460

25 Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala  
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Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr  
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30 Arg Tyr

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